

Figure 1 (A)

GGATCGTCTCAGGTCAGCGGAGGGA 25
 SL33
GGAGACTTATAGACCTATCCAGTCT 50
 TCAAGGTGCTCCAGAAAGCAGGAGT 75
 TGAAGACCTGGGTGTGAGGGACACA 100
 TACATCCTAAAAGCACCACAGCAGA 125
 GGAGGCCCAGGCAGTGCCAGGAGTC 150
 AAGGTTCCCAGAAGACAAACCCCCT 175
 AGGAAGACAGGCGACCTGTGAGGCC 200
CTAGAGCACCACTTAAGAGAAGAA 225
 SL34
 GAGCTGTAAGCCGGCCTTTGTCAGA 250
 GCCATCATGGGGGACAAGGATATGC 275
 CTACTGCTGGGATGCCGAGTCTTCT 300
 CCAGAGTTCCTCTGAGAGTCCTCAG 325
 AGTTGTCCTGAGGGGGAGGACTCCC 350
 AGTCTCCTCTCCAGATTCCCCAGAG 375
 TTCTCCTGAGAGCGACGACACCCTG 400
 TATCCTCTCCAGAGTCCTCAGAGTC 425
 GTTCTGAGGGGGAGGACTCCTCGGA 450
 TCCTCTCCAGAGACCTCCTGAGGGG 475
 AAGGACTCCCAGTCTCCTCTCCAGA 500
 TTCCCCAGAGTTCTCCTGAGGGCGA 525
 CGACACCCAGTCTCCTCTCCAGAAT 550
 TCTCAGAGTTCTCCTGAGGGGAAGG 575
 ACTCCCTGTCTCCTCTAGAGATTTC 600
 TCAGAGCCCTCCTGAGGGTGAGGAT 625
 GTCCAGTCTCCTCTGCAGAATCCTG 650
 CGAGTTCCTTCTTCTCCTCTGCTTT 675
 ATTGAGTATTTTCCAGAGTTCCCCT 700

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Figure 1(B)

GAGAGAACTCAGAGTACTTTTGAGG	725
GTTTTCCCCAGTCTCCTCTCCAGAT	750
TCCTGTGAGCTCCTCCTCCTCCTCC	775
ACTTTATTGAGTCTTTTCCAGAGTT	800
CCCCTGAGAGAACTCAGAGTACTTT	825
TGAGGGTTTTCCCCAGTCTCTTCTC	850
CAGATTCCTATGACCTCCTCCTTCT	875
CCTCTACTTTATTGAGTATTTTCCA	900
GAGTTCTCCTGAGAGTGCTCAAAGT	925
ACTTTTGAGGGTTTTCCCCAGTCTC	950
CTCTCCAGATTCCTGGGAGCCCCTC	975
CTTCTCCTCCACTTTACTGAGTCTT	1000
TTCCAGAGTTCCCCTGAGAGAACTC	1025
ACAGTACTTTTGAGGGTTTTCCCCA	1050
GTCTCCTCTCCAGATTCCTATGACC	1075
TCCTCCTTCTCCTCTACTTTATTGA	1100
GTATTTTCCAGAGTTCTCCTGAGAG	1125
TGCTCAAAGTACTTTTGAGGGTTTT	1150
CCCCAGTCTCCTCTCCAGATTCCTG	1175
GGAGCCCCTCCTTCTCCTCCACTTT	1200
ACTGAGTCTTTTCCAGAGTTCCCCT	1225
GAGAGAACTCACAGTACTTTTGAGG	1250
GTTTTCCCCAGTCTCCTCTCCAGAT	1275
TCCTATGACCTCCTCCTTCTCCTCT	1300
ACTTTATTGAGTATTTTACAGAGTT	1325
CTCCTGAGAGTGCTCAAAGTGCTTT	1350
TGAGGGTTTTCCCCAGTCTCCTCTC	1375
CAGATTCCTGTGAGCTCCTCTTTCT	1400

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Figure 1(C)

CCTACACTTTATTGAGTCTTTTCCA	1425
GAGTTCCCCTGAGAGAACTCAGAGT	1450
ACTTTTGAGGGTTTTCCCCAGTCTC	1475
CTCTCCAGATTCCTGTGAGCTCCTC	1500
CTCCTCCTCCTCCACTTTATTGAGT	1525
CTTTTCCAGAGTTCCCCTGAGTGTA	1550
CTCAAAGTACTTTTGAGGGTTTTCC	1575
CCAGTCTCCTCTCCAGATTCCTCAG	1600
AGTCCTCCTGAAGGGGAGAATACCC	1625
ATTCTCCTCTCCAGATTGTTCCAAG	1650
TCTTCCTGAGTGGGAGGACTCCCTG	1675
TCTCCTCACTACTTTCCTCAGAGCC	1700
CTCCTCAGGGGGAGGACTCCCTATC	1725
TCCTCACTACTTTCCTCAGAGCCCT	1750
CCTCAGGGGGAGGACTCCCTGTCTC	1775
CTCACTACTTTCCTCAGAGCCCTCA	1800
GGGGGAGGACTCCCTGTCTCCTCAC	1825
TACTTTCCTCAGAGCCCTCCTCAGG	1850
GGGAGGACTCCATGTCTCCTCTCTA	1875
CTTTCCTCAGAGTCCTCTTCAGGGG	1900
GAGGAATTCCAGTCTTCTCTCCAGA	1925
GCCCTGTGAGCATCTGCTCCTCCTC	1950
CACTCCATCCAGTCTTCCCCAGAGT	1975
TTCCCTGAGAGTTCTCAGAGTCCTC	2000
CTGAGGGGCCTGTCCAGTCTCCTCT	2025
CCATAGTCCTCAGAGCCCTCCTGAG	2050
GGGATGCACTCCCAATCTCCTCTCC	2075
AGAGTCCTGAGAGTGCTCCTGAGGG	2100

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Figure 1 (D)

GGAGGATTCCCTGTCTCCTCTCCAA	2125
ATTCCTCAGAGTCCTCTTGAGGGAG	2150
AGGACTCCCTGTCTTCTCTCCATTT	2175
TCCTCAGAGTCCTCCTGAGTGGGAG	2200
GACTCCCTCTCTCCTCTCCACTTTC	2225
CTCAGTTTCCTCCTCAGGGGGAGGA	2250
CTTCCAGTCTTCTCTCCAGAGTCCT	2275
GTGAGTATCTGCTCCTCCTCCACTT	2300
CTTTGAGTCTTCCCCAGAGTTTCCC	2325
TGAGAGTCCTCAGAGTCCTCCTGAG	2350
GGGCCTGCTCAGTCTCCTCTCCAGA	2375
GACCTGTCAGCTCCTTCTTCTCCTA	2400
CACTTTAGCGAGTCTTCTCCAAAGT	2425
TCCCATGAGAGTCCTCAGAGTCCTC	2450
CTGAGGGGCCTGCCCAGTCTCCTCT	2475
CCAGAGTCCTGTGAGCTCCTTCCCC	2500
TCCTCCACTTCATCGAGTCTTTCCC	2525
AGAGTTCTCCTGTGAGCTCCTTCCC	2550
CTCCTCCACTTCATCGAGTCTTTCC	2575
AAGAGTTCCCCTGAGAGTCCTCTCC	2600
AGAGTCCTGTGATCTCCTTCTCCTC	2625
CTCCACTTCATTGAGCCCATTAGT	2650
GAAGAGTCCAGCAGCCCAGTAGATG	2675

SL26

<u>AATATACAAGTT</u> CCTCAGACACCTT	2700
GCTAGAGAGTGATTCCTTGACAGAC	2725
AGCGAGTCCTTGATAGAGAGCGAGC	2750
CCTTGTTCACTTATACTGGATGA	2775
AAAGGTGGACGAGTTGGCGCGGTTT	2800

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Figure 1(E)

CTTCTCCTCAAATATCAAGTGAAGC	2825
SL27	
AGCCTATCACAAAGGCAGAGATGCT	2850
GACGAATGTCATCAGCAGGTACACG	2875
GGCTACTTTCCTGTGATCTTCAGGA	2900
AAGCCCGTGAGTTCATAGAGATACT	2925
TTTTGGCATTTCCTTGAGAGAAGTG	2950
GACCCTGATGACTCCTATGTCTTTG	2975
TAAACACATTAGACCTCACCTCTGA	3000
GGGGTGTCTGAGTGATGAGCAGGGC	3025
ATGTCCCAGAACCGCCTCCTGATTC	3050
TTATTCTGAGTATCATCTTCATAAA	3075
GGGCACCTATGCCTCTGAGGAGGTC	3100
ATCTGGGATGTGCTGAGTGGAATAG	3125
GGGTGCGTGCTGGGAGGGAGCACTT	3150
TGCCTTTGGGGAGCCCAGGGAGCTC	3175
CTCACTAAAGTTTGGGTGCAGGAAC	3200
ATTACCTAGAGTACCGGGAGGTGCC	3225
CAACTCTTCTCCTCCTCGTTACGAA	3250
TTCCTGTGGGGTCCAAGAGCTCATT	3275
CAGAAGTCATTAAGAGGAAAGTAGT	3300
AGAGTTTTTTGGCCATGCTAAAGAAT	3325
ACCGTCCCTATTACCTTTCCATCCT	3350
CTTACAAGGATGCTTTGAAAGATGT	3375
GGAAGAGAGAGCCCAGGCCATAATT	3400
GACACCACAGATGATTCGACTGCCA	3425
CAGAAAGTGCAAGCTCCAGTGTCAT	3450
GTCCCCCAGCTTCTCTTCTGAGTGA	3475
AGTCTAGGGCAGATTCTTCCCTCTG	3500

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Figure 1(F)

AGTTTGAAGGGGGCAGTCGAGTTTC	3525
TACGTGGTGGAGGGCCTGGTTGAGG	3550
CTGGAGAGAACACAGTGCTATTTGC	3575
ATTTCTGTTCCATATGGGTAGTTAT	3600
GGGGTTTACCTGTTTTACTTTTGGG	3625
TATTTTTCAAATGCTTTTCCTATTA	3650
ATAACAGGTTTAAATAGCTTCAGAA	3675
TCCTAGTTTATGCACATGAGTCGCA	3700
CATGTATTGCTGTTTTTCTGGTTTA	3725
AGAGTAACAGTTTGATATTTTGTA	3750
AAACAAAAACACACCCAAACACACC	3775
ACATTGGGAAACCTTCTGCCTCAT	3800
TTTGTGATGTGTCACAGGTTAATGT	3825
GGTGTTACTGTAGGAATTTTCTTGA	3850
AAGTGTGAAGGAAGTCTGCAGTTAA	3875
ATAGTGGAATAAAGTAAAGGATTGT	3900
TAATGTTTGCATTTTCCTCAGGTCCT	3925
TTAGTCTGTTGTTCTTGAAAATAA	3950
AGATACATACCTGGTTTGCTTGGCT	3975
TACGTAAGAAAGTAGAAGAAAGTAA	4000
ACTGTAATAAATAAAAAAAAAAAAA	4025
AAAAAA	4031

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exon I
CCATTCTGAGGGACGGCGTA GAGTTGGCCGAAGGAACCT GACCAGGCTCTGTGAGGAG GCAAGlgag//.....c
[exon I] intron I [exon I]
CTCAGGTCAGGGGAGGAGG 27

//clg gagicccaggaaaccaggcag lgaggccllggf-----c lgagacagtalctcagglc
AGACTTATAGACCTATCCAG TCTTCAAAGl//...//cag [GTGCTCCAGAAGCAGGAGT TGAAGACCTGGGTGTGAGGG ACACATACATCTAAAGCA 115
[exon II] intron II [exon II]
acagagcagaggalgcacag ggllgccagcaglglaagt ll.....gccclgaalgca caccaaggccccaccclgcc acaggacacatalaggacacca
CCACAGCAGAGGAGGCCAG GCAGTGCCAGGAGTCAAGl gaglgcacgacctgaciglg laccaaggccglaccccc gaacaglgtcagaccclggc
intron II exon II
cagaglcggccclaccclcc clactglcaglcclglagaa lcgac-clcglcggccggc lglaaccclga-glaccclcl cactlccclcttcagGTTTT 70
agcaccggccclglagccac ccactglcalclclgglgcc lcatggclcglccglcccagc lgtgccccgaggltgcltcl cgcglcclcttacagGTTCC 158
intron III exon III
caggggacagggccaacccag AGGACAGGATTCCCTGGAGG CCACAGAGGAGCACCC....A AGGAGAAGATCTglaaglag gcctllglttagagtlcclcaa
CAGAAGACAACCCCCTAGG AAGACAGGCGACCTGTGAGG CCTAGAGCACCCACCTTAAG AGAAGAAGAGCTGTAGCCG GCCTTTGTCTCAGAGGCCATCAT M 1
introns III
ggllcag-tlclcagclgag gccclcacacacclccclcl clccc-cagGCCTGTGGGTC TTCATTG-CCCAGCTCCTGC CCACACTCCTGCCTGCTGCC 188
GGlgagllclcagclgag gccactlggcaciglcclcl clcccaglcclglggat cccalcalacclattcglgt lcacacglllacclgclgt
on III G intron III
M S L E Q R S L H C K P E A L E A Q Q E A L G L V C V 28
1 CT--GACGAGAGTCATG TCCTTGAGCAGAGGAGTCT GCACTGCAAGCCTGAGGAAG CCCTTGAGGCCCCAACAGAG GCCCTGGGCTGCTGCTGTGT 286
1 cclgaacaatalcalcalg cclclctllclaaaccllcc agccccagclllagcaag gcllccagaaggcaatlilc alaciggagllggtagalc
1 O A A T S S S S P L V L G T L E E V P T A G S T D P P Q S P Q G A 61
1 GCAGGCTGCCACCTCCTCT CCTCTCCTCTGGTCTGGGC ACCCTGGAGGAGGTGCCAC TGCTGGTCAACAGATCCTC CCCAGAGTCTCAGGGAGGCC 386
1 agaggalccccc-----
S A F P T T I N F T R Q R Q P
TCGGCCTTCCCACTACCAT CAACTTCACTCGACAGAGGC AACCC-----gatgaggaagaggag gaagcllccclccallilic llcclcllccaccllllat
76 431

FIG. 2(B)

.....
 lccccgcccccccggt lllctllctcaccacalc cctctcctcgcctcgcgll cccaggggacaaaggatatg cctactgctgggatgccgag 294
 intron III D K D M P T A G M P S 13
 exon IV

.....
 TCTTCTCCAGAGTTCTCTG AGATCCTCAGAGTTGTCTT GAGGGGAGGAGTCCAGTC TCCTCTCCAGATTCCTCCAGAC GTTCTCTGAGAGCGGACGAC 394
 L L O S S E S P Q S Y P E G E D S Q S P L O I P Q S S P E S D D 46

.....
 ACCCTGTACTCTCCAGAG TCCTCAGAGTCGTTCTGAGG GGGAGGACTCCTCGGATCCT CTCAGAGACCTCCTGAGGG GAAGGACTCCAGTCTCCTC 494
 T L Y P L Q S P Q S R S E G E D S S D P L Q R P P E G K D S Q S P L 80

.....
 TCCAGATTCCTCCAGAGTTCT CCTGAGGGGACGACACCCA GTCTCCTCTCCAGAATCTC AGATTCTCTGAGGGGAAG GACTCCCTGTCTCCTCTAGA 594
 Q I P Q S S P E G D D T Q S P L Q N S Q S S P E G K D S L S P L E 113

.....
 GATTCTCAGAGCCCTCCTG AGGTGAGGATGTCAGTCT CCTCTGCAGAATCCTCGGAG TTCCTTCTCTCCTCTGCTT TATTGAGTATTTCCAGAGT 694
 I S Q S P P E G E D V Q S P L Q N P A S S F F S S A L L S I F Q S 146

.....
 TCCCCTGAGAGTATTCAAAG TCCTTTTGAGGGTTTCCCC AGTCGTCTCCAGATTCCT GTGAGCGCGCCCTCCTCCTC CACTTTAGTGAGTATTTCC 794
 S P E S I Q S P F E G F P Q S V L Q I P V S A A S S S T L V S I F Q 180

.....
 AGAGTCCCCTGAGAGTACT CAAAGTCCTTTTGAGGGTTT TCCCAGTCTCCACTCCAGA TTCCTGTGAGCGGCTCCTTC TCCTCCACTTTATGAGTAT 894
 S S P E S T Q S P F E G F P Q S P L Q I P V S R S F S S T L L S I 213

.....
 TTCCAGAGTCCCCTGAGA GAAGTCAGAGAACTTCTGAG GGTTTGACAGATCTCCTCT CCAGATTCCTGTGAGCTCCT CCTCGTCCCTCCACTTTACTG 994
 F Q S S P E R S Q R T S E G F A Q S P L Q I P V S S S S S T L L 246

A1
C1 AGTCTTTCCAGATTCCTTCC TGAGAGAACTCAGAGTACTT TTGAGGGTTTCCCCAGTCT CCACTCCAGATTCTCTGTGAG CCGCTCCTTCTCCTCCACTT 1094
S L F Q S S P E R T Q S T F E G F P Q S P L Q I P V S R S F S S T L 280

A1
C1 TATTGAGTATTTCCAGAGT TCCCCTGAGAGAACTCAGAG TACTTTTIGAGGGTTTGGCC AGTCTCCTCCTCCAGATTCT GTGAGCTCCTCCTCCTCCCTC 1194
L S I F Q S S P E R T Q S T F E G F A Q S P L Q I P V S S S S S S 313

A1
C1 CACTTATTGAGTCTTTCC AGAGTCCCCTGAGAGAACT CAGAGTACTTTTIGAGGGTTT TCCCAGTCTCTCCTCCAGA TTCTATGACCCTCCTCCTTCTC 1294
T L L S L F Q S S P E R T Q S T F E G F P Q S L L Q I P M T S S F 346

A1
C1 TCTCTACTTTTATGAGTAT TTCCAGAGTCTCCTGAGA GTCTCAAGTACTTTTIGAG GGTTTCCCCAGTCTCCTCT CCAGATTCTGGGAGCCCTT 1394
S S T L L S I F Q S S P E S A Q S T F E G F P Q S P L Q I P G S P S 380

A1
C1 CCTCTCCTCCTTACTG AGTCTTTCCAGAGTCTCCCTGAGAGAACTCAGAGTACTT TTGAGGGTTTCCCCAGTCT CCTCTCCAGATTCTCTAIGAC 1494
F S S T L L S L F Q S S P E R T H S T F E G F P Q S P L Q I P M T 413

A1
C1 CTCCTCCTTCTCCTCCTTACTT TATTGAGTATTTTACAGAGT TCTCTGAGAGTCTCAAAG TGCTTTTIGAGGGTTTCCCTC AGTCTCCTCCTCAGATTCTT 1594
S S F S S T L L S I L Q S S P E S A Q S A F E G F P Q S P L Q I P 446

A1
C1 GTGAGCTCCTCTTCTCCTCA CACTTATTGAGTCTTTTCC AGAGTCCCCTGAGAGAACT CAGAGTACTTTTIGAGGGTTT TCCCAGTCTCCTCCTCAGAGA 1694
V S S S F S Y T L L S L F Q S S P E R T Q S T F E G F P Q S P L O I 480

A1
C1 TCTCTGAGGCTCCTCCTCC TCTCTCCTCCTTATTGAG TCTTCTCAGAGTCTCCCTG AGTGTACTCAAGTACTTTT GAGGGTTTCCCCAGTCTCC 1794
P V S S S S S S T L L S L F O S S P E C T Q S T F E G F P Q S P 513

A1
C1 TCTCCAGATTCTCAGAGTC CTCCTGAAGGGGAGAATACC CATTCTCTCTCCAGATTGT TCCAAGTCTTCCGAGTGGG AGGACTCCCTGTCTCCTCAC 1894
L Q I P Q S P P E G E N T H S P L Q I V P S L P E W E D S L S P H 546

A1
C1 TACTTCTCAGAGCCCTCC TCAGGGGGAGGACTCCCTAT CTCCTCAGTCTTCTCCTCAG AGCCCTCTCAGGGGAGGA CTCCTGTCTCCTCCTACT 1994
Y F P Q S P P Q G E D S L S P H Y F P Q S P P Q G E D S L S P H Y F 580

A1
C1 TTCTCAGAGCCCTCAGGGG GAGGACTCCCTGTCTCTCA CTACTTCTCAGAGCCCTC CTCAGGGGGAGGACTCCAIG TCTCTCTCTACTTCTCTCA 2094
P Q S P Q G E D S L S P H Y F P Q S P P Q G E D S M S P L Y F P Q 613

A1
C1 GAGTCTCTCAGGGGAGG AATCCAGTCTTCTCTCCAG AGCCCTGAGCATCTGCTC CTCCTCCACTCCATCCAGTC TTCCCAGAGTTTCCCTGAG 2194
S P L Q G E E F Q S S L Q S P V S I C S S S T P S S L P Q S F P E 646

A1
C1 AGTTCTCAGAGTCTCTGA GGGGCTGTCCAGTCTCTC TCCATAGTCTCAGAGCCCT CCTGAGGGGATCAGACTCCCA ATCTCTCTCAGAGTCTCTG 2294
S S Q S P P E G P V Q S P L H S P Q S P P E G M H S Q S P L Q S P E 680

A1
C1 AGAGTCTCTCAGGGGAG GATTCCTGTCTCTCTCCA AATCTCAGAGTCTCTTG AGGAGAGGACTCCCTGTCT TCTCTCCATTTCTCCTCAGAG 2394
S A P E G E D S L S P L Q I P Q S P L E G E D S L S S L H F P Q S 713

A1
C1 TCTCTGAGTGGGAGGACT CTTCTCTCTCTCTCCTCTT CCTCAGTTTCTCTCTCAGG GGAGGACTTCCAGTCTCTC TCCAGAGTCTGTGAGTATC 2494
P P E W E D S L S P L H F P Q F P P Q G E D F Q S S L Q S P V S I 746

A1
C1 TGCTCTCTCTCCTCTCTT GAGTCTTCCCAGAGTTTCC CTGAGAGTCTCTCAGAGTCT CCTGAGGGGCTCTCAGTC TCTCTCCAGAGACCCTGTC 2594
C S S T S L S L P Q S F P E S P Q S P P E G P A Q S P L Q R P V S 780

A1
C1 GCTCTCTCTCTCTCTACT TTAGCGAGTCTCTCTCAAG ITCCCATGAGAGTCTCTCAGA GTCTCTCAGGGGCTGCTGCC CAGTCTCTCTCTCAGAGTCC 2694
S F F S Y T L A S L L Q S S H E S P Q S P P E G P A Q S P L Q S P 813

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FIG. 2(E)

A1
C1 TGTGAGCTCCTTCCCTCCTTCC CAGAGTTCTCTGTGAGCTC CTTCCTCCTCCTCCACTTCAT CGAGTCTTCCCAAGAGTTCC 2794
[V_S_S_F_P_S_S_T_S_S_L_S_Q_S_S_P][V_S_S_F_P_S_S_T_S_S][S_L_S_K_S_S] 846

A1
C1 CCTGAGAGTCTCTCCAGAG TCCTGTGATCTCTTCTCCTT CCTCCACTTCATTGAGCCCA TTCAGTGAAGAGTCCAGCAG CCGTGAAGAGGAGGGGCCAA 468
P E S P L Q S P [V_I_S_F_S_S_S_T_S_L_S_P_S][S E E S S S P V D E Y T S 880
S E G S S S R E E E G P S 89
AGTGAGGGTTCAGCAG

A1
C1 GTTCTCAGACACCTTGCTA GAGAGTGATCTCTTGACAGA CAGCGAGTCTCTTGATAGAGA GCGAGCCCTTGTTCACTTAT ACACCTGGATGAAAAGGTGGA 2994
S S D T L L E S D S L T D S E S L I E S E P L F T Y T L D E K V D 913
E S L F R A V I T K K V A 108
GAGTCTTGTTCCGAGCA

A1 GCACCTCTTGATCTCTG...
C1 GTTCTCAGACACCTTGCTA GAGAGTGATCTCTTGACAGA CAGCGAGTCTCTTGATAGAGA GCGAGCCCTTGTTCACTTAT ACACCTGGATGAAAAGGTGGA 2994
S S D T L L E S D S L T D S E S L I E S E P L F T Y T L D E K V D 913
D L V G F L L L K Y R A R E P V T K A E M L E S V I K N Y K H C F 140
TGATTTGGTTGGTTTCTGC TCCTCAAAATATCGAGCCAGG GAGCCAGTCAACAAGGCAGA AATGCTGGAGAGTGTCAICA AAAATTACAAGCACTGTTTT 623
C1 CGAGTTGGCGGGTTTCTTC TCCTCAAAATATCAAGTGAAG CAGCCTATCAACAAGGCAGA GATGCTGACGAATGTCAICA GCAGGTACACGGGCTACTTT 3094
E L A R F L L L K Y Q V K Q P I T K A E M L T N V I S R Y T G Y F 946

A1
C1 P E I F G K A S E S L Q L V F G I D V K E A D P T G H S Y V L V T C 174
CCTGAGATCTTCGCAAGC CTCTGAGTCTCTTGACGCTGG TCTTGGCAATGACGTGAAG GAAGCAGACCCCAACCGGCA CTCCTATGTCCTTGTACCT 723
C1 CCTGTGATCTTCAGGAAAGC CCGTGAGTTCATAGAGATAC TTTTGGCATTTCCCTGAGA GAAGTGGACCT...GAIGA CTCCTAIGTCTTTGTAAACA 3191
P V I F R K A R E F I E I L F G I S L R E V D P . D D S Y V F V N T 979

A1
C1 L G L S Y D G L L G D N Q I M P K T G F L I I V L V M I A M E G G 207
GCCTAGGTCTCTCCTATGAT GGCCTGCTGGGTGATAATCA GATCATGCCCCAAGACAGGCT TCCTGATAATTGCTCTGGTC ATGATTGCAATGGAGGGCGG 823
C1 CATTAGACCTCACCTCTGAG GGGTGTCTGAGTATGAGCA GGGCATGTCCAGAACCGCC TCCTGATCTTATTCIGAGT ATCATCTTCATAAAGGGCAC 3291
L D L T S E G C L S D E O G M S Q N R L L I L I L S I I F I K G T 1012

A1
C1 H A P E E E I W E E L S F H E V Y D G R E H S A Y G E P H K L L T 240
CCATGCTCTGAGGAGGAAA TCTGGGAGGAGCTGAGTGTG ATGGAGGTGATGATGGGAG GGAGCAGATGCTTATGGGG AGCCAGGAGAGCTGCTCACC 923
C1 CTAGCCCTCAGGAGGATCA TCTGGGATGTCTGAGTGA -TAGGGGTGCTGCTGAGGAG GGAGCAGTTCCTTGGGG AGCCAGGAGGAGCTCCTCACT 3391
Y A S E E V I W D V L S G I G V R A G R E H F A F G E P R E L L T 1015

FIG. 2(F)

O D L V Q E K Y L E Y R Q V P D S D P A R Y E F L W G P R A L A E T 274
 CAAGATTGGTGCAGGAAA GTACCTGGAGTACCGGAGG TGCCGGACAGTATCCCGCA CGCTATGAGTTCCTGTGGG TCCAAGGGCCCTCGCTGAAA 1023
 AAAGTTGGGTGCAGGAACA TTACCTAGAGTACCGGGAGG TGCCCAACCTCTCTCTCTCT CGTTACGAATTCCTGTGGG TCCAAGAGCTCATTGAGAAG 3491
 < V W V Q E H Y L E Y R E V P N S S P P R Y E F L W G P R A H S E V 1079

S Y V K V L E Y V I K V S A R V R F F P S L R E A A L R E E E 307
 "CAGCTATGIGAAAGTCTT GAGTATGTGATCAAGGTGAG TGCAAGAGTTCGCTTTTCT TCCCATCCCTGCGTGAAGCA GCTTTGAGAGAGGAGGAAGA 1123
 TCATTAAGAGGAAAGTAGTA GAGTTTTGGCCATGCTAAA GAATACCGTCCCTATTACCT TTCCATCCTCTTACAAGGAT GCTTTGAAAGATGTGGAAGA 3591
 I K R K V V E F L A M L K N T V P I T F P S S Y K D A L K D V E E 1112

G V OPA 309
 3GGAGTCTGAGCATGAGTTG CAGCAAGGCCAGTGGGAGG GGGACTGGCCAGTGCACCT TCCAGGGCCGCGTCCAGCAG CTTCCTCCCTCGCTGTGAC 1223
 GAGAGCCAGGCCATAATTG ACACCACAGATGATTCGACT GCCACAGAAAGTGCAAGCTC CAGTGTGATGTCCCCAGCT TCTCTTCTGAGTGAAGTCTA 3691
 R A Q A I I D T T D D S T A T E S A S S V M S P S F S S E OPA 1142

...ATGAGGCCCATCTTCA CTCTGAAGAGAGCGGTGAGT GTTCTCAGTAGAG-..... GTTTC 1279
 GGGCAGATTCTCCCTCTGA GTTTGAAGGGGGCAGTCGAG TTCTACGTGTGGAGGGCC TGGTTGAGGCTGGAGAGAAC ACAGTGTCTATTGCAATTTCT 3791

TGTTCTATTGGGTGACTGG AGATTATCTTTGTTCTCTT TTGGAATTGTTCAAAAGTTT TT--TTTTAAGGGATGGTTG AATGAACCTTCAGCATCCAAG 1377
 GTTCCATATGGGTAGTATG GGGTTACCTGTTTACTTT TGGTATTTTCAAAAGCTT TTCCATTAATAACAGGTTT AAATAGCTTCAGAAATCCTAG 3891

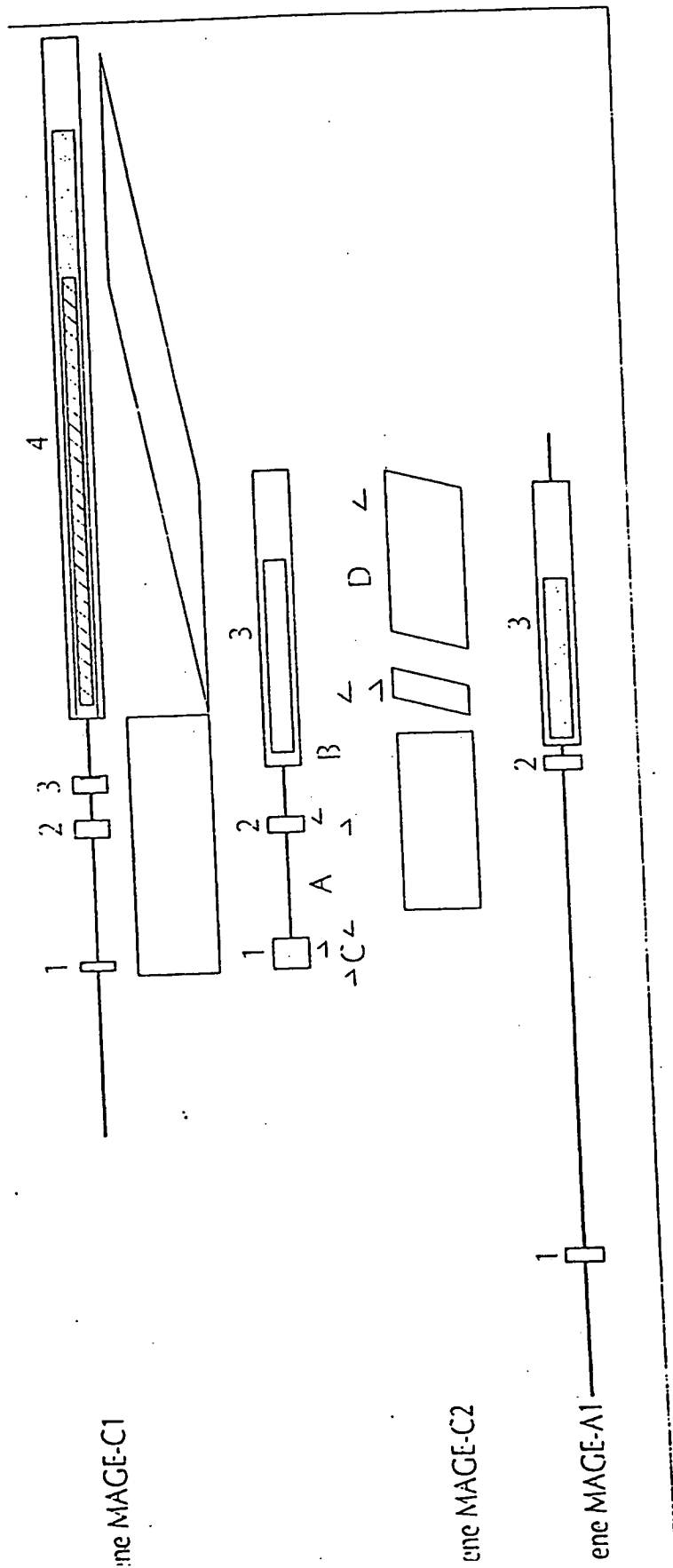
TTTATGAATGACAGCAGT-C ACACAGTCTGTGTATATAG TTTAAGGGTAAGAGTCTTGT GTTTTATCAGATTGGGAAA TCCATTCTATTTTGTGAATT 1476
 TTTATGCACATGAGTCCGAC ATGTATTGCTGTTTTCTGG TTTAAGAGTAACAGTTTGTAT ATTTTGTAATAACAAAAACA CACCCAAACACACACCATTTG 3991

GGGATAATAACAGCAGTGGG ATAAGTACTTAGAATGTGA AAAATGAGCAGTAAATAGA TGAGATAAAGAACTAAAGAA ATTAAGAGATAGTCAATTTCT 1576
 GGAAACCTTCTGCCTCAT TGTGATGTCACAGGTTA ATGTGTTACTGTAGGAA TTTTCTTGAAACTGTGAAGG AACCTCTGCAGTTAAATAGTG 4091

TGCCTTATACCTCAGTCTAT TCTGTAAAATTTTAAAGAT ATATGCATACCTGGATTCC TTGGCTTCTTTGAGAAATGTA AGAGAAATTAATCTGAATA 1676
 GAATAAAGTAAAGGATTGT AATGTTGCAATTCCTCAGG TCCTTAGTCTGTTGTTCTT GAAAACCTAAAGATACATACC TGGTTTGTCTGGCTTACGTA 4191

AAGAATTCCTCTGT-----
 AGAAAGTAGAAGAAAGTAAA CTGTAATAAATAAA 1691
 4225

FIG. 4



5

10

[illegible]

25

30

Figure 6 Amino-acid sequence of the putative MAGE-C3
protein (SEQ ID NO: 22)

	MPLFPNLPRLSFEEDFQNPSVTEDLVDAQDSIDEEEDASSTSSSSFHFL	50
5	FPSSSSLSSSSPLSSPLPSTLILGVPEDEDMPAAGMPPLPQSPPEIPPQG	100
	PPKISPQGPPQSPQSPLDSCSSPLLWTRLDEESSSEEDTATWHALPES	150
	ESLPRYALDEKVAELVQFLLLKYQTKEPVTKAEMLTTVIKKYKDYFPMIF	200
	GKAHEFIELIFGIALTDMDPDNHSYFFEDTLDLTYEGSLIDDQGMPKNCL	250
	LILILSMIFIKGSCVPEEVIWEVLSAIGVCAGREHFIYGDPRKLLTIHWV	300
10	QRKYLEYREVPNSAPPRYEFLWGPRAHSEASKRSLRVFIQAIQYHP	346

10085108.030102

Figure 7 Nucleotide sequence of gene MAGE-B5
(SEQ ID NO: 23)

This sequence is the antiparallel sequence corresponding to nucleotides 123358 to 124185 of BAC clone 466O4 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL189 and SL190 that were used in the RT-PCR assay are indicated.

10 ATGACTTCTGCAGGTGTTTTTAATGCAGGATCTGACGAAAGGGCTAACAG 50
TAGAGATGAGGAGTACCCATGTTCTCAGAGGTCTCACCCTCCACTGAGA 100
GTTTCATGCAGCAATTTTCATAAATATTAAGGTGGGTTTGTGGAGCAGTTC 150
CTGCTCTACAAGTTCAAAATGAAACAGCGTATTTTGAAGGAAGATATGCT 200
GAAGATTGTCAACCCAAGATACCAAACAGTTTGTCTGAGATTACACAGAA 250
15 GAGCTTCTGAGCACATTGAGGTTGTCTTTGCAGTTGACTTGAAGGAAGTC 300
AACCCAACCTTGTCACTTATATGACCTTGTCTGAGCAAGCTGAAACTCCCCAA 350
CAATGGGAGGATTTCATGTTGGCAAAGTGTTACCCAAGACTGGTCTCCTCA 400
SL189
TGACTTTCCTGGTTGTGATCTTCCTGAAAGGCAACTGTGCCAACAAGGAA 450
20 GATACCTGGAAATTTCTGGATATGATGCAAATATATGATGGGAAGAAGTA 500
CTACATCTATGGAGAGCCCAGGAAGCTCATCACTCAGGATTTCTGTGAGGC 550
TAACGTACCTGGAGTACCACCAGGTGCCCTGCAGTTATCCTGCACACTAT 600
CAATTCCTTTGGGGTCCAAGAGCCTATACTGAAACCAGCAAGATGAAAGT 650
CCTGGAATATTTGGCCAAGGTCAATGATATTGCTCCAGGTGCCTTCTCAT 700
SL190
25 CACAATATGAAGAGGCTTTGCAAGATGAGGAAGAGAGCCCAAGCCAGAGA 750
TGCAGCCGAACTGGCACTACTGCAGTGGCCAAGACTGTCTCAGGGCGAA 800
GTTTCAGCAGCTTCTCTCAACCCTATTGA 828

30

Figure 8 Amino-acid sequence of the putative MAGE-B5
protein (SEQ ID NO: 24)

	MTSAGVFNAGSDERANSRDEEYPCSSSEVSPSTESSCSNFINIKVGLLEQF	50
5	LLYKFKMKQRILKEDMLKIVNPRYQNQFAEIHRRASEHIEVVFAVDLKEV	100
	NPTCHLYDLVSKLKLPNNGRIHVGKVLPKTGLLMTFLVVI FLKGNCANKE	150
	DTWKFLDMMQIYDGKKYIYGEPRKLITQDFVRLTYLEYHQVPCSYPAHY	200
	QFLWGPRAYTETSKMKVLEYLAKVNDIAPGAFSSQYEEALQDEEESPSQR	250
	CSRNWHYCSGQDCLRAKFSSFSQPY	275

10

1005108.030102
201009.0805001

Figure 9 Nucleotide sequence of gene MAGE-B6
(SEQ ID NO: 25)

This sequence is the antiparallel sequence corresponding to nucleotides 146417 to 147640 of BAC clone 466O4 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL191 and SL192 that were used in the RT-PCR assay are indicated.

1005106.070102

10	ATGCCTCGGGGTCACAAGAGTAAGCTCCGTACCTGTGAGAAACGCCAAGA	50
	GACCAATGGTCAGCCACAGGGTCTCACGGGTCCCCAGGCCACTGCAGAGA	100
	AGCAGGAAGAGTCCCACTCTTCCTCATCCTCTTCTCGCGCTTGTCTGGGT	150
	SL191	
	GATTGTCGTAGGTCTTCTGATGCCTCCATTCTCAGGAGTCTCAGGGAGT	200
	GTCACCCACTGGGTCTCCTGATGCAGTTGTTTCATATTCAAATCCGATG	250
	TGGCTGCCAACGGCCAAGATGAGAAAAGTCCAAGCACCTCCCGTGATGCC	300
	TCCGTTCTCAGGAGTCTCAGGGAGCTTACCCACTGGCTCTCCTGATGC	350
	AGGTGTTTCAGGCTCAAATATGATGTGGCTGCCAACGGCCAAGATGAGA	400
	AAAGTCCAAGCACTTCCCATGATGTCTCCGTTCTCAGGAGTCTCAGGGA	450
	GCTTACCCACTGGCTCGCCTGATGCAGGTGTTTCAGGCTCAAATATGA	500
	TGTGGCTGCCGAGGGTGAAGATGAGGAAAGTGTAAGCGCCTCACAGAAAG	550
	SL192	
	CCATCATTTTTAAGCGCTTAAGCAAAGATGCTGTAAAGAAGAAGGCGTGC	600
	ACGTTGGCGCAATTCTGTCAGAAAGTTTGAGAAGAAAGAGTCCATTTT	650
25	GAAGGCAGACATGCTGAAGTGTGTCCGCAGAGAGTACAAGCCCTACTTCC	700
	CTCAGATCCTCAACAGAACCTCCCAACATTTGGTGGTGGCCTTTGGCGTT	750
	GAATTGAAAGAAATGGATTCCAGCGGCGAGTCTACACCCTTGTCAGCAA	800
	GCTAGGCCTCCCCAGTGAAGGAATTCTGAGTGGTGATAATGCGCTGCCGA	850
	AGTCGGGTCTCCTGATGTCGCTCCTGGTTGTGATCTTCATGAACGGCAAC	900
30	TGTGCCACTGAAGAGGAGGTCTGGGAGTTCTGGGTCTGTTGGGGATATA	950
	TGATGGGATCCTGCATTCAATCTATGGGGATGCTCGGAAGATCATTACTG	1000
	AAGATTTGGTGCAAGATAAGTACGTGGTTTACCGGCAGGTGTGCAACAGT	1050
	GATCCTCCATGCTATGAGTTCCTGTGGGGTCCACGAGCCTATGCTGAAAC	1100
	CACCAAGATGAGAGTCCTGCGTGTTTTGGCCGACAGCAGTAACACCAGTC	1150
35	CCGGTTTATACCCACATCTGTATGAAGACGCTTTGATAGATGAGGTAGAG	1200
	AGAGCATTGAGACTGAGAGCTTAA	1224

Figure 10 Amino-acid sequence of the putative MAGE-B6 protein (SEQ ID NO: 26)

	MPRGHKSKLRTCEKRQETNGQPQGLTGPQATAEKQEESHSSSSSSSRACLG	50
5	DCRRSSDASIPQESQGVSPDAGVVSYSKSDVAANGQDEKSPSTSRDA	100
	SVPQESQGASPTGSPDAGVSGSKYDVAANGQDEKSPSTSHDVSVVPQESQG	150
	ASPTGSPDAGVSGSKYDVAAEGEDEESVSASQKAIIFKRLSKDAVKKKAC	200
	TLAQFLQKKFEKKESILKADMLKCVRREYKPYFPQILNRTSQHLVVAFGV	250
	ELKEMDSSGESYTLVSKLGLPSEGILSGDNALPKSGLLMSLLVVIFMNGN	300
10	CATEEEVWEFLGLLGIYDGILHSIYGDARKIITEDLVQDKYVVYRQVCNS	350
	DPPCYEFLWGPRAYAETTKMRVLRVLADSSNTSPGLYPHLYEDALIDEVE	400
	RALRLRA	407

10085108.030102